



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
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 - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTG	ACT	TGGA	ACG	AGAC	GAC	CTG	CTCT	GTG	ACAGG	CATGA	GGGGT	CCCCG	GCAGAG	56		
ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG	AGC	CCA	AAT	TCC	TCC	CTG	TTG	CTG	104
Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu	
1				5					10					15		
CTG	TTG	CTG	CTG	CTG	AGT	CCT	TGC	CTG	CGG	GGG	ACA	CCT	GAC	TGT	TAC	152
Leu	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr	
				20				25					30			
TTC	AGC	CAC	AGT	CCC	ATC	TCC	TCC	AAC	TTC	AAA	GTG	AAG	TTT	AGA	GAG	200
Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu	
		35					40					45				
TTG	ACT	GAC	CAC	CTG	CTT	AAA	GAT	TAC	CCA	GTC	ACT	GTG	GCC	GTC	AAT	248
Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	
	50					55					60					
CTT	CAG	GAC	GAG	AAG	CAC	TGC	AAG	GCC	TTG	TGG	AGC	CTC	TTC	CTA	GCC	296
Leu	Gln	Asp	Glu	Lys	His	Cys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala	
65					70				75						80	
CAG	CGC	TGG	ATA	GAG	CAA	CTG	AAG	ACT	GTG	GCA	GGG	TCT	AAG	ATG	CAA	344
Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	
				85					90					95		
ACG	CTT	CTG	GAG	GAC	GTC	AAC	ACC	GAG	ATA	CAT	TTT	GTC	ACC	TCA	TGT	392
Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys	
			100					105					110			
ACC	TTC	CAG	CCC	CTA	CCA	GAA	TGT	CTG	CGA	TTC	GTC	CAG	ACC	AAC	ATC	440
Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	
		115					120					125				
TCC	CAC	CTC	CTG	AAG	GAC	ACC	TGC	ACA	CAG	CTG	CTT	GCT	CTG	AAG	CCC	488
Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro	
	130					135					140					

TGT	ATC	GGG	AAG	GCC	TGC	CAG	AAT	TTC	TCT	CGG	TGC	CTG	GAG	GTG	CAG	536
Cys	Ile	Gly	Lys	Ala	Cys	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Val	Gln	
145					150					155					160	
TGC	CAG	CCG	GAC	TCC	TCC	ACC	CTG	CTG	CCC	CCA	AGG	AGT	CCC	ATA	GCC	584
Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala	
				165					170					175		
CTA	GAA	GCC	ACG	GAG	CTC	CCA	GAG	CCT	CGG	CCC	AGG	CAG	CTG	TTG	CTC	632
Leu	Glu	Ala	Thr	Glu	Leu	Pro	Glu	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu	
			180					185					190			
CTG	CTG	CTG	CTG	CTG	CCT	CTC	ACA	CTG	GTG	CTG	CTG	GCA	GCC	GCC	TGG	680
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp	
		195					200					205				
GGC	CTT	CGC	TGG	CAA	AGG	GCA	AGA	AGG	AGG	GGG	GAG	CTC	CAC	CCT	GGG	728
Gly	Leu	Arg	Trp	Gln	Arg	Ala	Arg	Arg	Arg	Gly	Glu	Leu	His	Pro	Gly	
	210					215					220					
GTG	CCC	CTC	CCC	TCC	CAT	CCC	TAGGATT	CGA	GCCTT	GTG	GCA	TCGTT	GACTC			779
Val	Pro	Leu	Pro	Ser	His	Pro										
225					230											
AGCCAGGGTC	TTATCTCGGT	TACACCTGTA	ATCTCAGCCC	TTGGGAGCCC	AGAGCAGGAT											839
TGCTGAATGG	TCTGGAGCAG	GTCGTCTCGT	TCCAGTCGAC													879

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu	
1				5					10					15		
Leu	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr	
			20					25					30			
Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu	
		35					40					45				
Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	
	50					55					60					
Leu	Gln	Asp	Glu	Lys	His	Cys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala	
65					70					75					80	
Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	
			85						90					95		
Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys	
			100					105					110			

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
 115 120 125
 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
 130 135 140
 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
 145 150 155 160
 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
 165 170 175
 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
 180 185 190
 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
 195 200 205
 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
 210 215 220
 Val Pro Leu Pro Ser His Pro
 225 230

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT	TCCGGGGCCC	CCGGCCGAA	ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG		53				
			Met	Thr	Val	Leu	Ala	Pro	Ala	Trp						
			1				5									
AGC	CCA	ACA	ACC	TAT	CTC	CTC	CTG	CTG	CTG	CTG	AGC	TCG	GGA	CTC	101	
Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Ser	Gly	Leu		
	10					15				20						
AGT	GGG	ACC	CAG	GAC	TGC	TCC	TTC	CAA	CAC	AGC	CCC	ATC	TCC	TCC	GAC	149
Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	
	25				30					35					40	
TTC	GCT	GTC	AAA	ATC	CGT	GAG	CTG	TCT	GAC	TAC	CTG	CTT	CAA	GAT	TAC	197
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	
			45						50					55		
CCA	GTC	ACC	GTG	GCC	TCC	AAC	CTG	CAG	GAC	GAG	GAG	CTC	TGC	GGG	GGC	245
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	
			60					65					70			
CTC	TGG	CGG	CTG	GTC	CTG	GCA	CAG	CGC	TGG	ATG	GAG	CGG	CTC	AAG	ACT	293
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	
		75					80					85				
GTC	GCT	GGG	TCC	AAG	ATG	CAA	GGC	TTG	CTG	GAG	CGC	GTG	AAC	ACG	GAG	341
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	
	90					95					100					
ATA	CAC	TTT	GTC	ACC	AAA	TGT	GCC	TTT	CAG	CCC	CCC	CCC	AGC	TGT	CTT	389
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	
105					110					115					120	
CGC	TTC	GTC	CAG	ACC	AAC	ATC	TCC	CGC	CTC	CTG	CAG	GAG	ACC	TCC	GAG	437
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	
				125					130					135		
CAG	CTG	GTG	GCG	CTG	AAG	CCC	TGG	ATC	ACT	CGC	CAG	AAC	TTC	TCC	CGG	485
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	
		140						145					150			
TGC	CTG	GAG	CTG	CAG	TGT	CAG	CCC	GAC	TCC	TCA	ACC	CTG	CCA	CCC	CCA	533
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	
		155					160						165			

TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581
 Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
 170 175 180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
 Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
 185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
 205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
 220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC 774
 Val Glu His
 235

GCAGTGAGAC AGACATCTAT CATCCCATT TACAGGGGAG GATACTGAGG CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80

Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110

Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu
 180 185 190
 Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
 195 200 205
 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
 210 215 220
 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
 225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60
 ACTTCAGCCA C 71

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37